REMARKS

The Specification Amendments

As requested by the Examiner, applicants have amended the paragraph spanning pages 10 and 11 of the specification to insert sequence identifiers for the sequences on page 10, line 33 and page 11, line 1. Applicants also have corrected the spelling of co-segregation in this paragraph. Consistent with this amendment, applicants have amended the Sequence Listing to add sequences that are present on pages 10 and 11 of the specification as filed, which were inadvertently omitted from the Sequence Listing filed March 26, 2001. In addition, applicants have amended the Sequence Listing to list the inventors as applicants (field <110>), to add the file reference (field <130>), to insert references to the instant application (fields <140> and <141>), and to insert reference to the Japanese priority application (fields <150 and <151>). No other changes to the Sequence Listing have been made.

As also requested by the Examiner, applicants have amended the paragraph spanning pages 9 and 10 to insert the complete citation for Ohtsuki (1990). Applicants have enclosed a copy of this reference and an English translation thereof as Exhibit A.

None of these amendments adds new matter. Their entry is requested.

The Claim Amendments

Applicants have amended claims 1 and 14 to delete reference to an amino acid sequence with at least 80% homology to SEQ ID NO: 2. Applicants have amended claim 13

to depend from claim 12 not cancelled claim 2. Support for this amendment appears, for example, on page 7, lines 9-20 and in SEQ ID NO: 1.

None of these amendments adds new matter. After entry of the amendments, claims 1 and 12 – 16 will be pending.

The Claim Objections

The Examiner has objected to former claim 13 as being dependent from a canceled claim. Applicants have amended claim 13 to depend from claim 12, thus obviating the objection.

The Specification Objections

The Examiner has objected to the specification for not incorporating SEQ ID NO:s when referring to nucleic acid or amino acid sequences. The Examiner states that an assigned sequence identifier is required in all instances where the description or claims of a patent application discuss sequences and draws the applicants' attention to page 10, line 33 and page 11, line 1.

Applicants have amended page 10, line 33 and page 11, line 1 to insert the appropriate sequence identifiers, thus obviating the objection. This amendment also required an amended Sequence Listing.

The Examiner has objected to the specification for not including a complete citation when referencing a document and draws the applicants' attention to page 9, lines 27 – 29.

Applicants have amended page 9, lines 27 – 29 to insert the complete citation, thus obviating the objection.

The Rejection under 35 U.S.C. § 101

The Examiner has rejected claims 1 and 12 – 16 under 35 U.S.C. § 101, as lacking either a substantial asserted utility or a well established utility. The Examiner asserts that there is no clear nexus between applicants' invention of SEQ ID NO: 1 and any utility set forth so as to allow one skilled in the art at the time the invention was made to take the claimed invention and clearly and immediately achieve the benefits set forth. The Examiner cites Walbot (1992 Annu. Rev. Plant Physiol. Plant Mol. Biol. 43: 49-82) and contends that the mutant plant must be complemented with a wild-type allele of the suspected gene to properly ascertain that the mutant gene is responsible for a particular phenotype. The Examiner states that one of skill in the art would not know for certain the identity of the gene responsible for the dwarf phenotype.

In addition, the Examiner states that it is not clear how one skilled in the art should use a nucleic acid encoding SEQ ID NO: 2 to control growth promotion, yield increase, quality improvement, maturation enhancement, or tolerance against biotic and abiotic stresses. The Examiner contends that it would require more than routine experimentation to determine how to use the claimed invention. Finally, the Examiner states that claims drawn to sequences having 80% homology to SEQ ID NO: 2 would lack utility. Applicants traverse in view of the claims, as amended.

First, applicants have amended claims 1 and 14 to delete reference to sequences having 80% homology to SEQ ID NO: 2, thus obviating this aspect of the rejection.

Second, applicants strongly disagree with the Examiner's contention that the specification does not provide a clear nexus between SEQ ID NO: 1 and its utility in studying and controlling the brassinosteroid response. Quite to the contrary, applicants have provided scientifically convincing evidence that a plant with a mutation in the gene comprising SEQ ID NO: 1 exhibits a dwarf phenotype. Specifically, applicants have shown that:

(1) the phenotypes of dwarfism, upright form and malformation of grain hulls genetically cosegregated with a Tos17-retrotransposon insertion in the gene comprising SEQ ID NO: 1 (Example 2);

(2) that a separately generated plant line with a Tos17 retrotransposon inserted at a different site in the same gene exhibits all of the same phenotypes (Example 3);

(3) that the phenotypes in both plant lines are associated with a loss of expression of the gene comprising SEQ ID NO: 1 (Example 4); and

(4) that the mutation is associated with insensitivity to the brassinosteroid hormone brassinolide (Example 6).

Therefore, contrary to the Examiner's assertions, one skilled in the art provided with this evidence would reasonably conclude that mutation of the gene comprising SEQ ID NO: 1 results in brassinolide-insensitivity and the phenotypes described.

Walbot, in fact, acknowledges that a combination of methods utilizing the "sequence [flanking the insertion] as a hybridization probe can be used to build a convincing case that a clone represents the gene of interest." (p. 69). These methods include expression

analysis (p. 69) and obtaining additional mutants (p. 70) — the exact methods applicants have used. Walbot further acknowledges that co-segregation is "evidence . . . that the band in question [i.e., the one into which a transposon had inserted] defines the gene of interest." (p. 64). Indeed, in view of this evidence, the Examiner has acknowledged that it is reasonable to conclude that the polypeptide of SEQ ID NO: 2 (encoded by SEQ ID NO: 1) has some functionality in the response of rice plants to brassinolide (October 3, 2004 Office Action, p. 5). Thus, one of skill in the art would conclude that a mutation in the gene comprising SEQ ID NO: 1 is responsible for the dwarf phenotype.

Finally, applicants disagree with the Examiner assertion that it is not clear how one skilled in the art should use a nucleic acid encoding SEQ ID NO: 2. In addition to the ways well known to one of skill in the art as described in applicants' previous responses (i.e. cosuppression or antisense), the specification explicitly teaches at least one way to use the nucleic acid molecule of the invention to create a plant with a mutation in the gene comprising the nucleic acid sequence. Specifically, the specification teaches mutagenesis by activation of a retrotransposon to produce a population of plant lines with random retrotransposon insertions (Example 1) and use of the nucleic acid molecule of the invention (i.e. primers derived therefrom) to screen that population by PCR for a plant line with a transposon insertion in the corresponding gene (Example 3). As demonstrated by Walbot, both transposon mutagenesis and PCR were well within the skill in the art at the time the application was filed. Thus, one of skill in the art would at least know this means of using the claimed nucleic acid molecule to produce a dwarf plant.

Accordingly, one of skill in the art would recognize that the nucleic acids of the invention can be used to produce dwarf plants and would know how to use them for this purpose. These dwarf plants are research tools to study the brassinosteroid response. Alternatively, dwarf plants have a well established utility in commercial horticulture. Furthermore, as described in applicants' December 31, 2003 Amendment and Response, this utility is asserted in the instant specification. Accordingly, the invention recited in pending claims 1 and 12 – 16 has a specific, substantial and credible utility and the rejection should be withdrawn.

The Rejections under 35 U.S.C. § 112, First Paragraph

The Examiner has rejected claims 1 and 12 – 16 under 35 U.S.C. 112, first paragraph, as lacking either a substantial asserted utility or a well established utility. The Examiner states that one skilled in the art would not know how to use the claimed invention and that undue experimentation would be required to use the invention. Applicants traverse.

As described above, the polynucleotides of the present invention can be used to produce plants that have mutations in the genes comprising the polynucleotides and that such plants would exhibit dwarfism, upright form, and malformation of grain hulls and/or be brassinosteroid insensitive. Accordingly, one of ordinary skill in the art could use the claimed polynucleotides to genetically engineer plants with the desired phenotypes with no more than routine experimentation.

The Examiner also has rejected claims 1 and 12 – 16 under 35 U.S.C. § 112, first paragraph, as lacking written description. Specifically, the Examiner states that

applicants do not identify essential regions of the protein encoded by SEQ ID NO: 1 or any polynucleotide sequences that encodes a polypeptide with at least 80% homology to SEQ ID NO: 2 that encodes a functional protein. The Examiner contends that in the absence of this disclosure applicants have failed to describe a representative number of polynucleotides to support the breadth of the claim.

As described above, applicants have amended claims 1 and 15 to delete reference to at least 80% homology, thus obviating this rejection.

The Rejection under 35 U.S.C. § 112, Second Paragraph

The Examiner has rejected former claims 1 and 12 – 16 under 35 U.S.C. 112, second paragraph, as lacking enablement. The Examiner states that applicants have not taught by way of disclosure or example how to use the claimed sequence to produce an agronomically useful plant and contends that brassinosteroid signaling is poorly understood. The Examiner also states that applicants have not taught how to make or isolate any of the sequences in the broad claims or which regions of SEQ ID NO: 1 can be used to amplify any of said polynucleotides. The Examiner contends that one of skill in the art cannot predict which polynucleotides encoding a polypeptide with at least 80% homology to SEQ ID NO: 2 will encode a protein with the same activity. Applicants traverse in view of the claims, as amended.

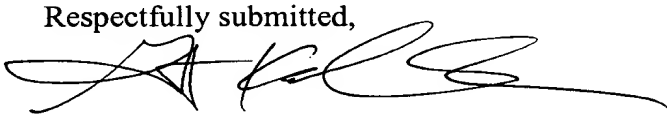
As described above, applicants have amended claims 1 and 15 to delete reference to at least 80% homology, thus obviating this aspect of the rejection. Furthermore, contrary to the Examiner's assertion, applicants have explicitly taught by way of example

how the claimed nucleic acid sequence may be used to produce a useful plant. Specifically, as described above, applicants have demonstrated that a nucleic acid of the invention can be used to produce a plant with a mutation in the gene comprising the nucleic acid sequence. Applicants have further shown that one of skill in the art would reasonably expect such a plant to exhibit a dwarf phenotype. Accordingly, the rejection under 35 U.S.C. § 112, second paragraph, should be withdrawn.

Conclusion

For the reasons presented above, applicants request that the Examiner allow claims 1 and 12 – 16 to issue.

Respectfully submitted,



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